

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/575,361DATE: 06/07/96  
TIME: 09:43:18

INPUT SET: S10941.raw

## SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

## (1) GENERAL INFORMATION:

(i) APPLICANT: Chandrasegaran, Srinivasan

(ii) TITLE OF INVENTION: A GENERAL METHOD TO CLONE HYBRID  
RESTRICTION ENDONUCLEASES USING lig GENE

(iii) NUMBER OF SEQUENCES: 35

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cushman Darby &amp; Cushman L.L.P.

(B) STREET: 1100 New York Avenue, NW, Ninth Floor, East  
Tower

(C) CITY: Washington

(D) STATE: DC

(E) COUNTRY: USA

(F) ZIP: 20005-3918

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/575,361

(B) FILING DATE: 20-DEC-1995

(C) CLASSIFICATION: 435

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kokulis, Paul N.

(B) REGISTRATION NUMBER: 16,773

(C) REFERENCE/DOCKET NUMBER: PNK/4130/213779/DJP

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-861-3000

(B) TELEFAX: 202-822-0944

(C) TELEX: 6714627 CUSH

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

format  
error  
throughout**Explanation of error that occurred throughout the Sequence Listing:**

For all of your nucleic acid and amino acid sequences, the text at the end of each line "wrapped" down to the next line. This occurred if your file was retrieved in a word processor after creating it in PatentIn. Your word processor probably has different margin settings than those used in PatentIn. (A right margin set at least to .3 in your word processor will prevent wrapping). Please submit your original ".app" file that can be found in the /patentin/projects subdirectory.

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/575,361DATE: 06/07/96  
TIME: 09:43:21

INPUT SET: S10941.raw

51  
52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
53  
54 Tyr Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa  
55 Leu 1 5 10 15 Leu  
56  
57  
58  
59 Xaa Xaa His Xaa Xaa Xaa His  
60 20  
61  
62 (2) INFORMATION FOR SEQ ID NO:2:  
63  
64 (i) SEQUENCE CHARACTERISTICS:  
65 (A) LENGTH: 24 amino acids  
66 (B) TYPE: amino acid  
67 (D) TOPOLOGY: linear  
68  
69  
70  
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
72  
73 Tyr Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa  
74 Leu 1 5 10 15  
75  
76  
77  
78 Xaa Xaa His Xaa Xaa Xaa Xaa His  
79 20  
80  
81 (2) INFORMATION FOR SEQ ID NO:3:  
82  
83 (i) SEQUENCE CHARACTERISTICS:  
84 (A) LENGTH: 25 amino acids  
85 (B) TYPE: amino acid  
86 (D) TOPOLOGY: linear  
87  
88  
89  
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
91  
92 Tyr Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa  
93 Leu 1 5 10 15  
94  
95  
96  
97 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His  
98 20 25  
99  
100 (2) INFORMATION FOR SEQ ID NO:4:

*sample of amino acid "wraps"*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/575,361DATE: 06/07/96  
TIME: 09:43:47

INPUT SET: S10941.raw

451 (2) INFORMATION FOR SEQ ID NO:23:

452

453

(i) SEQUENCE CHARACTERISTICS:

454

(A) LENGTH: 74 base pairs

455

(B) TYPE: nucleic acid

456

(C) STRANDEDNESS: single

457

(D) TOPOLOGY: linear

458

459

460

461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

462

463

CUCGACCAAA CCUAGGUUCG AAGGGCCCCU UCUUAAGCUC CUCCGAGAGC UCCAGCUGAA

464

465

466

GGAGAUCCUCC AUGG

467

468

469

(2) INFORMATION FOR SEQ ID NO:24:

470

471

(i) SEQUENCE CHARACTERISTICS:

472

(A) LENGTH: 87 base pairs

473

(B) TYPE: nucleic acid

474

(C) STRANDEDNESS: double

475

(D) TOPOLOGY: linear

476

477

478

479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

480

481

GGATCCAAAGC TTAGCGATCT GCCTGCAGGT CGACTCTAGC CAGGGGCGGG GTGGTCTAGT

482

483

484

ATCGTTCAAT GATACTTCAT GGAATTC

485

486

487

(2) INFORMATION FOR SEQ ID NO:25:

488

489

(i) SEQUENCE CHARACTERISTICS:

490

(A) LENGTH: 23 base pairs

491

(B) TYPE: nucleic acid

492

(C) STRANDEDNESS: single

493

(D) TOPOLOGY: linear

494

495

496

497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

498

499

CCCCCTGAAGG AGATATACAT ATG

500

Sample of  
nucleic acid  
wraps.

60

74

60

87

23

Entire  
listing  
not  
shown.  
(Just these  
two sample  
pages)

08/575,361

## Notice of Availability

### Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR 18230) on May 1, 1990, and in the *PTO Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the *PTO Official Gazette*.

The software can be accessed/requested in the following locations:

- 1) Dial-up access to the Patent and Trademark Office Bulletin Board System.  
Phone number: 703-305-8950  
Cost: Free-of-charge
- 2) Dial-up access through the Internet. FTP site: ftp.uspto.gov  
Login as "anonymous". Software is in directory /pub/checker  
Cost: Free-of-charge
- 3) For diskette copies, telephone requests to 703-306-2600.  
Cost: \$25.00

For Further Information Contact: Meredith Beckhardt at 703-308-421